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Result
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                               609.8
188.8
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1 actgcatcagcccactctct.....aanaaaaaaaaaaaaaaa 2144
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Copyright (c) 1993 - 2000 Compugen Ltd
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         BH487741 BOGWB48TR
ALD80416 Arabidops
BM270448 Sak13a03.
BH477964 BOHKJ17TR
BH465017 BOHN433TR
AZ686821 ENTLI74TR
AL514901 AL514901
AL106171 Drosophil
BE420736 HWM002 A0
                                                                                                                 BH530370 BOGDQ70TF
BF291837 WHE2204_E
B12531 F1C14-T7 IG
BH530380 BOGDQ70TR
BH62012 BOHNZ43TF
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63.8	63.8	64	64.2	64.2	64.2	64.2	64.6	65	65.2	65.2	65.2	65.4	65.4	65.6	65.6	65.6	65.6	65.8	65.8	66.2	6 7	67.2	67.4	67.6	67.6	67.8	67.8	
3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.1	3.1	3.1	3.1	3.1	3. 1	3.1	3.1	3.1	3.1	3.1	3.1	3.2	3.2	3.2	3. 2	
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RESULT B10183/c VERSION KEYWORDS COMMENT REFERENCE DEFINITION FEATURES SOURCE ACCESSION Locus TITLE ORGANISM AUTHORS JOURNAL source Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eurosids II; Brassicales; Brassicaceae; Arabidopsis. High quality sequence start: 87
High quality sequence stop: 806
Location/Qualifiers Unpublished (1997)
Other_GSSs: F19N12-T7
Contact: Ecker J. B10183 DNA linear GSS 14-MAY-1997 F19N12-Sp6 IGF Arabidopsis thaliana genomic clone F19N12, DNA Tel: 215-898-9384 Fax: 215-898-8780 Arabidopsis Thaliana Genome Center University of Pennsylvania BAC End Sequences at ATGC Feng, J., Dewar, K., Buehler, E., Kim, C., Li, Y., Shinn, P., Sun, H. B10183.1 GI:2091302 sequence Class: BAC ends Seq primer: Spb Email: jecker@atgenome.bio.upenn.edu thale cress (bases 1 to 1233) of Biology, University of Pennsylvania, Philadelphia, /organism="Arabidopsis thaliana" /strain="Columbia" /db_xref="taxon:3702" /clone="F19N12" /clone=lib="IGF" /sex="hermaphrodite" /note="Vector: BeloBACII; Site_1: EcoRI; Site_2: EcoRI; PA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1085 AATTTCAAGTTTCAGGCTTTTCGCCCGGGGAAAAGGGAAGGGATTTGTGGTGGGGGATT 1026
879 tcgatgatgagtcatctgagcaacgttcagagatatattcacagtattccgacttcgatt 938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1025 TTAAAGGGCAAACCCCGGGGCCCGAAACCCTTTTCCCGGGGGGAGGTCCCCGTTGAAAGGGA 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              579 cacgatocgatgtgaccttcgccggacatgtctccaacagccggagtttgaatttcgaat 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                819 tcggatgcgtctctgatctcgctttgctctgagaaattctcggaagaggtttcggattctc 878
                                                                                                                                                                                                            759 tcgtggaagctgattcctctcttggatcggccaaggaattgaagccggagcttgagatag 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                          545 CACGATCCGATGTGACCTTCGCCGGACATGTCTCCAACAGCCGGAGTTTGAATTTCGAAT 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      402 ttggtgattcgaaa---tttcgaaggattacgaggtcttactctaagctacacaaggaga 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      785 GGACTCTAATGGGAAGAGGAAGATTTCTAAAACCTGGTTATAAAGTGAAAGAGGACGA 726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     288 ctgatgacaacgttt-cctgtggttcgagcagagtcgagaagagct--cgaatccgaaga 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 28.4%; Score 609.8; DB 12; Length 1233; Local Similarity (母語) Pred. No. 9.3e-73; Length 1233; es 833; Conservative 0; Mismatches 149; Indels 25;
                                                                                          TCGGATGCGTCTCTGATCTCGCTTGCTCTGAGAAATTCTCGGAAGAGGTTTCGGATTCTC
                                                                                                                                                                                   TCGTGGAAGCTGATTCCTCTTTGGATCGGCCAAGGAATTGAAGCCGGAGCTTGAGATAG 306
                                                                                                                                                                                                                                                                         TCGGGAGCGTTACCGGAGGAGCTGATAACGAAGAATTGAAATCTCCAAGCCGAGCAGCT 366
                                                                                                                                                                                                                                                                                                  tcgggagcgttaccggaggagctgataacgaagaattgaaatctccaagccgagcagct 758
                                                                                                                                                                                                                                                                                                                                                                 CGGAGAATAAGGAGAGCGACGTCGTTTCTGTCATATCTGGAGTTGAGTACTGTTCCAAGT 426
                                                                                                                                                                                                                                                                                                                                                                                          cggagaataaggagagcgacgtcgtttctgtcatatctggagttgagtactgttccaagt 698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Source
                                                                                                                                                      121 TGCTTCTGTCGATTCCTGCTCCGATTTGCTAGCTGATGACAACGTTTCCTGTGGTTCGAG 180
                                                                                                                                                                          256 tgcttctgtcgattcctgctccgatttgctagctgatgacaacgtttcctgtgggttcgag 315
                                                                                                                                                                                                                                             196 acagatetetecegttettgttcaatcacetetetggagcaaacaaatoggagtetetetge 255
                                                                                                                                                                                                                                                                                                                   136 tgagccgacgccgttcgccgggaagaagctccggtcgacgcgattacgccggaagagagc 195
                                                                                         181 CAGAGTCGAGAA 192
                                                                                                                        316 cagagtcgagaa 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 8.8%; Local Similarity 99.0%;
                                                                                                                                                                                                                                                                                                 1 TTAGCCGACGCCGTTCGCCGGGAAGAAGCTACGGTCGACGCGATTACGCCGGAAGAGAGC 60
     BH530370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: rounsley@tigr.org
Seq primer: M13-21
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Steve Rounsley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l (bases 1 to 192)
Rounsley_S.D., Field,C.E., Bass,S., Linher,K., Linher,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
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B97951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="IGF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="F22C23"
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   818 bp
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GSS 14-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360 AACGAACTTCCATTTTCGAATTTGAAA - - TCTGAATTCGAATCTAAAACTTTCTTCGGAG 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 aacgaacttccattttcaaaattcgaatttctaatttctagtttcaagctttcgtacg-- 89
                                                                                                                                                                                                                                                                                                                                                                                                                                cgacgccgttcgccgggaagaagctccggtcgacgcgattacgccggaagagagcacaga 200
GATCATACTCTAAGCTAC-CAAGGAGAAGATCATAGATGAGACTGAAGCA
                   ggtcttactctaagctacacaaggagaaggaggagatgagatcgaagta 481
                                                                            GACCTGGTAAAGATGTAAAGAAGGAGACGATCGCTGATCCG-AAGTTCGGAGGATCACTA
                                                                                                  aacctggttataatgt---gaaggagacgattggtgattcgaaatttcgaaggattacga 431
                                                                                                                                                                                           gcagagtcgagaagagctcgaatccgaagaagactctaattgaagaggtagaagtttcta 374
                                                                                                                                                                                                                                      CCGTTGATTCCTGCTCCAATTTGCTCTCTGCAGTCGACGACAACGTTTCATGCGGTTCTA 656
                                                                                                                                                                                                                                                                          ctgtcgattcctgctccgatttgct-----agctgatgacaacgtttcctgtggttcga
                                                                                                                                                                                                                                                                                                                   TATCTCCAGTTTCTATCCAGCCACCTCTCT-GCCAAAGGAAGTAGGAGTATCCGCTGCTT
                                                                                                                                                                                                                                                                                                                                                                                           CGACGCCGTTCCCCGGGAAGAAGCTTCGATCGATTCCATCTCGCCGGAAGAGCGCTCAGA 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCAGAGTCGAGAAGAGCT-----TCGGGAAGAATCGAATTGAAGAGGAAGAAGTTTCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 818)
Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cdtown@tigr.org
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genomic DNA inserted into pHOS1 using BstXI linkers"
a    186 c    168 g    200 t
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1. .818
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/strain="TO1000bH3"
/db_xref="taxon:3712"
/clone="B0GDQ70"
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1430 gaagaaatcaaccttacaacagcatccggaaaaggaacttcaccattcagaacctaaga 1489
                                                                                                                                                                                                                                              1370 aaaagcgaaaggactctaatactagtcgggattgcgagtcttactctggccaccagaatt 1429
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                                                                                                                                                                                                 4 AAAGGCTCTAGGAATGTGCAGTTGCTGGGCATTGCCTGCATCACCCTAGCCACCCGCATT 63
                                                                                                   GAAGAGAACCAGCCATACAATAGCATCATGCAGAAGTCTTTCATGGTAGGGATCAACCTT 123
                                                                                                                                                                                                                                                                                                    280;
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WHEZZ04_E10_JZ0ZS Aegilops speltoides anther cDNA library Aegilops
speltoides cDNA clone WHEZ204_E10_JZ0, mRNA sequence.
BEZ91837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence have been trimmed to remove vector sequence quality sequence with phred score less than 20 Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genomes - Anther cDNA library from Aegilops speltoides
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Eukaryota; Viridiylantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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Site_1: EcoRI; Site_2: XhoI; Plants were grown in a growth
Chamber at the University of California, Davis (Akhunov).
Premeiotic anthers were harvested, total RNA and poly(A)
RNA were prepared, from each tissue and then pooled, a
CDNA library was made, and the CDNA clones were in vivo
excised to give pBluescript phagemids in the Ty Close lab
(Akhunov, Chin, Choi, Close, Fenton, Kianian, Otto, Simons
, Zhang) at the University of California, Riverside.
Plasmid DNA preparations and DNA sequencing were performed
in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /Clone="WHE2204_E10_J20"
/clone_lib-"Aegilops speltoides anther cDNA library"
/tissue_type-"Anther"
/dev_stage="Premeiotic anthers"
/lab_host="E. coli SOLR"
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/cultivar="F2 from 2-12-4-8-1-1-(1) x PI36909-12-811-(1
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61.5%;
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Pred. No. 1.8e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
Other_GSSs: F1C14-Sp6
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                                                                                                                                                                                                                                                                                                                                                                          Seq primer:
                                                                                                                                                                                                                                                                                                                                                                                      Email: jecker@atgenome.bio.upenn.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis Thaliana Genome Center University of Pennsylvania
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Ecker J.
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                                                                                                                                                                                                                                                                                                                          quality sequence start: 37 quality sequence stop: 889
                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   of Biology, University of Pennsylvania,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ., Dewar, K., Buehler, E.,
                                                                                                                                                  /clone_lib="IGF"
/sex="hermaphrodite"
/sex="hermaphrodite"
/note="Vector: BeloBACII; Site_1: EcoRI;
Produced by Thomas Altmann"
a 247 c 234 g 375 t 2 others
                                                                                                                                                                                                                                  /db_xref="taxon:3702"
/clone="F1C14"
                                                                                                                                                                                                                                                                 /organism="Arabidopsis thaliana"
/strain="Columbia"
                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                           86.8%;
                                                          Score 172.6; DB Pred. No. 3e-14; 0; Mismatches
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                                                                                                                                                                                                                                                                                   Local Similarity 69.0%;
                                                   AACTTCTTATGGTAAAAACCTCTATTACTATATTTTTCTGTTCCGAGACACATGCACAC 435
                                                                                                                       GCAATGGAGTGGCTGATTCTAGAAGTCCTCAACTTCAAATGCTTCTCACCCCACAATCTTT 495
                                                                                                                                        gcaatggagtggctggttcaagaagtcctcaaacttcaaatgcttcacaccccacaatcttc 1570
                                                                                                                                                                                          AGCATCCGGAAAAGGAACTTCTACATTGAGAACCTAAAGTATAGCCGTCATGAAGTGGTG 555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l (bases 1 to 803)
Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other_GSSs: BOGDQ70TF
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BH530380
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
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Class: sheared ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cdtown@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 301-838-352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Chris Town
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BOGDQ70TR BOGD Brassica
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                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                 /clone="BOGD070"
/clone=lib="BOGD"
/clone=lib="BOGD"
/clone="Yector: pHOS1; Site_1: BstXI; 2-3 kb sheared
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
a 128 c 181 g 253 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism-"Brassica oleracea"
/strain-"TO1000DH3"
/db_xref-"taxon:3712"
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1761 aggtcc 1766
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                                                                                                                                                                                                                                   Match 7.1%;
Local Similarity 88.7%;
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                                                                                                            ctgttacctcactatccgaccaaactcaactctgtttttggccctcaactgtagcagctg 1700
                                                                                                                                                           GGTTTTACCTAAAAGCTGCACGAGCCAATCCAGAAGTTGAAAAGAAAAGCGAGATCTTTGG 199
                                                            cactegtggttctcgcctgcatcgaacacaacaacaatctctgcataccaacgagtcataa 1760
                                                                                              CTATAACCTCACTATCCGATCACACTCAACTCTGTTTTTGGCCCCTCAACTGTCGCAGCCG
                                 GGCTTGTAGTTCTCGCCTGCAGTGAACACAACAAAATCTCAGCATACCAACGAGTCATAA
                                                                                                                                                                                                                      165;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
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BOHNZ43TF BOHN Brassica
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Other_GSSs: BOHNZ43TR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cdtown@tigr.org
DNA is from a doubled haploid provided
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 301-838-3523
Fax: 301-838-0208
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Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M
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/note-"Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"
a 70 c 116 g 153 t
                                                                                                                                                                                                                                                                                                                                                                            /organism-"Brassica oleracea"
| Strain-"T01000DH3"
| /db_xref-"taxon:3712"
| /clone-"BOHNZ43"
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Pred. No. 2e-11;
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les 324; Conserv
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Town.C.D., Van Aken.S., Utterback,T. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
Other_GSSs: BOGWB48TF
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BOGWB48TR BOGW Brassica oleracea genomic clone BOGWB48, DNA
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/clone_lib="BOGW"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"
a 168 c 196 g 175 t
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/strain="TO1000DH3"
/db_xref="taxon:3712"
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     Glycine max

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;

Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
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Arabidopsis thaliana genome survey sequence T7 end of BAC FIC14 of
GF library from strain Columbia of Arabidopsis thaliana, genomic
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Salanoubat,M., Choisne,N., Artiguenave,F., Brottier,P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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/clone="F1C14"
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/strain="Columbia"
/db_xref="taxon:3702"
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Pred. No. 1.3e-06;
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                       1812 tggactggttgcttgggcagtaagca 1837
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                                                                                              1752 gagtcataaaggtccatgttagaacaacagataacgagttgcctgaatgcgttaagagtc 1811
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This clone is available through: ResGen, Invitrogen Corp. South Memorial Parkway Huntsville, AL 35801 For further it call: (800)-533-4363 or contact: ccueresgen.com web site:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  www.resgen.com
Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
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                                                                                                                                                                        Tissue culture and library construction were performed by Francoise Thibaud-Nissen and Anu Khana (Lila Yodkin lab, University of Illinois)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from mRNA isolated
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DNA is from a doubled haploid
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/strain="TO1000DH3"
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Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
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1 (bases 1 to 791)
Loftus, B., Van Aken, S. and Fraser, C.
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                                              Entamoeba histolytica
Entamoeba histolytica
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/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"
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/db_xref="taxon:3712"
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
Fax: 301 838 3543
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HM1: MSS sheared DNA library
Unpublished (2000)
Contact: Brendan J Loftus
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Similarity 52.2%;
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/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
/note="Vector: phosphore; Installed Bst I; Constructed Bst I; Con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          caccatttgtgtcgctcatacacatttatttcttattttccctaattcattagactctca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GWTTAWAWWWAAATTAWAWWWTTGAAAAAAAAAAATTGTGAAAAAAAWATWWAAAATWTA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acaggitatcattactattacaaaaaacaaacaaaggiaagtaataagaactcciciac 1952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster genome survey sequence SP6 end of BAC BACNISC18 of DrosBAC library from Drosophila melanogaster (fruit
                                         fly), genomic survey sequence
AL106171
AL106171.1 GI:5620504
                                                                                                                                                                                                                          CNS0161D
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Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL514901.1 GI:12778394
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1 (bases 1 to 668)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Ecc RV sites of the pCMVSPORT 6
loned into the Not I and Ecc RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies, Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : filang@lifetch.com URL :

Tetra //filang@lifetch.com URL :

Tetra //filang@lifetch.co
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/db_xref="taxon:9606"
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                                                                             WWATWWTTWTWTTWWWTWWWTAATATTTTTWTTTTATWTAWAATWATATAAAAAW 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1225)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genoscope.
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone=lib="DrosBAC"
/clone="BACN15C18"
/note="end: SP6"
a 128 c 38 g ::
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Search completed: July 25, Job time: 6186 sec

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1117 78 78 70 68 67 67 65 65

132699 5204 349980

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Sequence

RESULT ACUU6917/c ACCESSION VERSION SOURCE ORGANISM REFERENCE DEFINITION KEYWORDS TITLE JOURNAL AUTHORS 1 (bases 1 to 132699)
Chao,O., Shinn,P., Dunn,P., Buehler,E., Kahn,S., Kim,C., Walker,M., Williams,S., Altafi,H., Araujo,R., Conn,L., Conway,A.B., Williams,S., Altafi,H., Araujo,R., Kremenetskala,I., Lenz,C., Gonzalez,A., Hansen,N.F., Huizar,L., Kremenetskala,I., Lenz,C., Li,J., Liu,S., Luros,S., Rowley,D., Schwartz,J., Toriumi,M., Vysotskaia,V., Yu,G., Davis,R.W., Federspiel,N.A., Theologis,A. and HTG I, complete sequence. AC006917 AC006917.6 GI:4757662 AC006917 132699 bp DNA linear PLN 28-JUN-2000 Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. Unpublished Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome Arabidopsis thaliana thale cress Ow Corner Could Brown ALIGNMENTS ON N

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB Query Ħ

Description

REFERENCE AUTHORS

Ecker, J.R

TITLE JOURNAL

REFERENCE AUTHORS

JOURNAL

REFERENCE

(bases 1

AUTHORS

COMMENT

TITLE JOURNAL

FEATURES

source

CDS

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Cheuk, R., Shinn, P., Brooks, S., Buehler, E., Chao, Q., Johnson-Hopson, C., Khan, S., Kim, C., Altafi, H., Bei, B., Chin, C., Chio, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N., Chiu, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N., Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, J., Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thaveri, A., Tortumi, M., Vaysberg, M., Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (28-JUN-2000) Arabidopsis thaliana Genome Center, bepartment of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, Pa 19104-6018, USA On May 7, 1999 this sequence version replaced gi:4731042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (25-FEB-1999) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA 3, (bases 1 to 132699)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (07-MAY-1999) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Sta
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                                                                                                                                                                                                                                              .8180)
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ECLIMNLAKAEQEVELVSEQNRELDRENRKFLRQCSAERSHGSNKFNKRKSIKMMSSP
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/product="F1086.4"
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/db_xref="GI:8778208"
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                     aagcgaatcgtcttgtgttgattcgaattctggtgctggattaaggagattgaatgtgaa 540
                                                                                                                                                                               GGTAGAAGTTTCTAAACCTGGTTATAATGTGAAGGAGACGATTGGTGATTCGAAATTTCG
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  AAGCGAATCGTCTTGTTTGATTCGAATTCTGGTGCTGGATTAAGGAGATTGAATGTGAA
                                                                                      TTCCTGTGGTTCGAGCAGAGTCGAGAAGAGCTCGAATCCGAAGAAGACTCTAATTGAAGA
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20800. .20887,20957. .21108,21188. .21356,21448. .21906
22006. .22275,22367. .22570,22840. .22917))
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/note="similar to acid phosphatase type 5 emb|CAB63938.1;
similar to EST gb|N96048.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLHRTDHEOSTNISDDTLDGLHHMIHKLKTERSVRFOKVDKHACNAILLFVTDYHFDA
LAFSPLSVQLKDVAGSLFELWNLMDTSQEERTKFASVSYVVRSSESDITEPNILSSET
IEQVSAEVDCFNKLKASRMKELVMKRRTELENLCRLAHIEADTSTSLEKSTALIDSGT
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SLKEKLAAVPMLEDLRLOKDEMKORVDI KAOLEKKSEI SGYSDOLNUKMVGSLAL
DEQDLTLRKLNEYOTHLRSIGKEKSDRLNKVLDYVNEVHTLCGVLGVDFGOTVSEVHP
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/product="F1086.10"
/protein_id="AAF79221.1"
/db_xref="G1:8778212"
/tanslation="MTY1YRDTKITTKSTIPFLIFFLFCFSNLSMATLKHKPVNLVFY
/YNLIIIFSSHSSTAELRRLLQPSKTDGTVSFLVIGDWGRRGSYNQSQVALQWGEIGE
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/protein_id="AAF79248.1"
/db_xref="GI:8778239"
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KLTRKQQEEEKRRYRDQKKMODLLIKRRESIYGSKPSPRRSNSVRKTNGYNGDASVPP
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/oroduct="F10B6.9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCTCGCTCTCTGTACCTCCAGTTCAAGGAACAGTTCTGTAGATCCACGATTCCCAACGA
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                                                                                                                                                                                                                                                               Olek,A., Piepenbrock,C. and Berlin,K. Diagnosis of diseases associated with Patent: WO 0200928-A 874 03-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 874 from Patent W00200928. AX345803
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                                                                                                                                                          /db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
72 c 1014 g 2655 t
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                                                          Score 78.4; DB 6;
Pred. No. 4.1e-08;
0; Mismatches 146;
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                                                                                      aagcaatcaaaaagaacaaaaaccctaaaacccaggacacagtatactccgataccaacac 1892
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                                                                                                                                                                                                                                                    /note-"chemically treated genomic DNA (Homo sapiens)-Original length of seq 1: 3.673778 <223>-split as follows.-seq 01.000.001 TO 0.349.980-seq 02 0.300.001 649.980-seq 03 600.001 949.980-seq 04 900.001 1.249.980-seq 06 1.500.001 1.249.980-seq 06 1.500.001 1.849.980-seq 07 1.800.001 2.149.980-seq 08 2.100.001 1.849.980-seq 07 1.800.001 2.149.980-seq 10 2.700.001 1.449.980-seq 09 2.400.001 2.749.980-seq 12 3.300.001 3.049.980-seq 13 3.000.001 3.349.980-seq 12 3.300.001 3.649.980-seq 13 3.600.001 3.673.778 <223>-original length of seq 2: 3.67378 <223>-split as follows.-seq 14 0.000.001 TO 0.349.980-seq 15 0.300.001 649.980-seq 16 600.001 949.980-seq 17 900.001 1.849.980-seq 18 1.200.001 1.549.980-seq 19 1.500.001 1.849.980-seq 20 1.800.001 1.549.980-seq 19 1.500.001 1.849.980-seq 20 1.800.001 2.449.980-seq 21 2.100.001 2.449.980-seq 22 2.400.001 2.449.980-seq 23 2.700.001 3.649.980-seq 24 3.000.001 3.349.980-seq 25 3.300.001 3.649.980-seq 26 3.600.001 3.673.778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   297214.1 GI:3955062
MEF-2 co-repressor; MITR gene.
African clawed frog.
Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kingdom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sparrow, D.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sparrow,D.B., Miska,E.A., Langley,E., Reynaud-Deonauth,S., Kotecha,S., Towers,N., Spohr,G., Kouzarides,T. and Mohun,T.J. MEF-2 function is modified by a novel co-repressor, MITR
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Amphibia; Barrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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1 (bases 1 to 4435)
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        /db_xref="SPTREMBL.09YGY4"
/db_xref="SPTREMBL.09YGY4"
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KEOKHEOORKEDEAERHROEOQLCHPRSKDRYKERAYASTEVROKLOEFILSKSANTE
PLTWATSHSMGRBPKLMYTAAHHTSLDQSSPPPSGTSPTYKCPPPGNQDDPPLRKTAS
PHIKVPSRLKOKYVERRSSPLLRKDSIYVSSYKRIFFYAABSSVSSSSPYSGPSSP
NNGPVAMBAEHETPEVLSYNIST ERLVUSHHLVHHERSLSLLMLYTSPSIPNITIGHA
TATOLNTSSSLKEQOKYDPQAPROGVSMAGQYAGGIPTSSNHYSLECKANSHQAILOH
LLLKEQMRQOKILASGGTPVLHQSPLAAKDRVSPAGRVAHKLPRHRPLHFTOSAPLPQ
STLAQLVIQOQHQOFLEKQKQYQQQIHMNKILSKSIEQLRGCHLEAEEDLHGDNL
MQEKSSSIDNTRSYSSTDLRTGFPGSYKVKEBPPDSENEIKTHLQSBOKSVFAQQVT"
89 a 866 c 806 g 1274 t
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                                                                                                                                                                                                                                               /product="MITR protein"
/protein_id="CAB10167.1"
/db_xref="GI:3955063"
                                                                                                                                                                                                                                                                                                                                                                                      /organism="Xenopus laevis"
/db_xref="taxon:8355"
121. .1818
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121. .1818
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Matches

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Similarity

3.38; 78.0%;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa chromosome 3 clone OSUNBa0081P02, *** SEQUENCING IN PROGRESS ***, 10 ordered pieces.
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Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wing, R.A., Yu, Y., Soderlund, C., Chen, M., Kim, H.-R., Rambo, T., Saski, C., Henry, D., Oates, R. and Simmons, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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1 (bases 1 to 149791)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by the finished sequence as soon as it is available and the accession number will be preserved.

1 1837: contig of 1837 bp in length gap of unknown length
1838 21394: contig of 19557 bp in length
                                                                                                  40949
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                                                                                            /clone="OSJNBa0081P02"
33193 c 33129 g 42
                                                                                                                                                        /organism="Oryza sativa"
/db_xref="taxon:4530"
                                                                                                                                                                                                 1. .14979
                                                                                                                                   /chromosome="3"
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                                                                                                                                                                                                                                   gap of unknown lengt
149791: contig of 448 bp in
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                                                                                                                                                                                                                                                                                                                     141457:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       116292:
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3.2%;
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scontig of 7296 bp in length
gap of unknown length
contig of 2153 bp in length
gap of unknown length
gap of unknown length
gap of 15716 bp in length
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Score 68.6; DB 2;
Pred. No. 1.1e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Draft entry and computer-readable sequence for [Mol. Cell. Biol. (1989) In press] kindly provided by R.H.Kessin, 23-MAR-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       discoideum contains three promoters specific for growth, aggregation, and late development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Faure, M., Franke, J., Hall, A.L., Podgorski, G.J. and Kessin, R.H. The cyclic nucleotide phosphodiesterase gene of Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The cyclic nucleotide phosphodiesterase gene of Dictyostelium discoideum utilizes alternate promoters and splicing for the synthesis of multiple mRNAs
MOLICELL Biol. 9 (9), 3938-3950 (1989)
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Podgorski, G.J., Franke, J., Faure, M. and Kessin, R.H.
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D.discoideum (strain NC4; cell line AX3-K) DNA, clones
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                                     join(3689.
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2267. .606
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join(1163. .1779,40
1163. .1779
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1780. .4
  3689.
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                                                                                          /note-"vegetative promoter"
2377. .4077
                                                                                                                                                                                                                                                                                                                                                             /organism="Dictyostelium discoideum"
/db_xref="taxon:44689"
                3689. .6060
/note="late promoter"
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Olek, A., Piepenbrock, C. and Berlin, K. Diagnosis of known genetic parameters within Patent: WO 0200932-A 9 03-JAN-2002;
                                                                                                                                                                                                                                           AX344558 349980 bp
Sequence 9 from Patent WO0200932
AX344558
                                                                                                                                                                              synthetic construct. synthetic construct
                                                                                                                                                                                                                             AX344558.1 GI:18492444
                                                                                Epigenomics AG (DE)
                                                                                                                                                          artificial sequence.
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SSFLITKKGSNLEIALDAGTVWGGVRLITFKYENILENITYESHVILEOGRESHFIK
NHVMSVETGHSHILDHVGLILIVASPEDVILAKNULDVOPEINGIMGLIMGLIGHEVDET
SSSILGKKTIMGLPSTINSISTNLENNQVWPNLPSFGRYQYESIASGIEYPETELVPY
NATTMSLVANEFPESVKVKPEELCHDNLISTSFLATDSLSGEGLAFFSDTGVPSSVAC
DMEGKIYAVWKGIKIDKLKAIYIETSFPNNTDDSAMFGHILPBRUVMKLMQLLVVSIG
TSPPMTNLKHVKLIIEHIKPQVAEDPNGWTTORVIYQQLKEANNNGVRIIIPNQGDPI
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4297. .>606
             /organism="synthetic construct"
/db_xref="taxon:32630"
                                                                Location/Qualifiers
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/protein_id="AAA63168.1"
/db_xref="GI:695313"
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/codon_start=1
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/EC_number="3.1.4.17"
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51.1%;
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Pred. No. 1.8e-05;
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                                                                                                                                                                                                                                                                                                                                          Eukaryota; Mycetozoa; Dictyostelium.

1 (bases 1 to 7736)

Rivero,F., Dislich,H., Glockner,G. and Noegel,A.A.

The Dictyostelium discoideum family of Rho-related procedure and control of the control of
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Dictyostelium discoideum
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Rivero, F., Dislich, H. and Noegel, A.A.
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Location/Qualifiers
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Pred. No. 2.6e-05;
0; Mismatches 148;
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/gene="colors to EST clones SSB614, SSG550, SSJ204
/note="corresponds to EST clones SSB614, SSG550, SSJ204
and SSK792 from the Japanese cDNA sequencing project; cDNA
(partial) already described in L11594."
/product="RacD"
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EIGLDEVSKFISDQARPDSYDNQKPLNDQKKSHNPFTLAGQLITANLSLVNIQMHVLE
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GYEPPSPPSSSSTTPITTSGBDTLQKSPTLQRKVAPPPQQQNEQDLPSSLVGKPPPLK
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LKKGDIIVVLAKDSSGWWQGINQSTQATGWFSNTFVEEIKEEKLPPPPSSSENKQPLK
IVKSPPPKSSSSSQPQTVEAKLQSLSDTPKLETARKAGAAKGRKPPSRVRASYLLSDD
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QINSIQLNSKQVSYLAATLANDGVCPFSQDLKLAPKNIISKTIDLIRICNSTPITSSI
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NSSSSSSSSNINSSGGFVAAKRESGAVUTQOROFKVLLNUROSTILSCVPAAIONEE
SSRINTTTTTUTVIPAVOPLIQLKPROTNTEINTSGNSIPATTSKESOSTKEESSSGGN
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/db_xref="GI:12007301"
/trans1ation="MFKWHQSNNLVYYTFNIPANVTKQDIHAEITSSSIGLGVKGFGL
   ALSLVFKLYSRVLK"
1097 c 837
                                                            EYKQILSFIKNSYVVAQVIRGLIKCVTSFWTSLTPNQKNDMKSNIWLYIESVQPLEQF
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LPBI NOTNGGTP I I LVCTKTDLREDKKTLSOLDESKOEPVSADESVALAKEIGAVOFF
ECSALTGNGVND I FAAA I KAAFNKPAVTSPTSKSSGKSSPSSTSSKPSKTTTTTTTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAG45121.1"
/db_xref="G1:12007302"
/translation="MAYGIKKTYKVYVYGDGAVGKTSLLILYTTKAFPKDYVPTVFDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Rho-GTPase;
of Rho proteins"
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                                                                                                                 /protein_id="AAG45122.1"
/db_xref="GI:12007303"
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join(7278. .7533,7645. .>7736)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Olek, A., Piepenbrock, C. and Berlin, K.
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                              /note="chemically treated genomic DNA (Homo sapions)-Original length of seq 1: 3.673778 223>-split as follows.-seq 01 0.000.001 To 0.349.980-seq 02 0.300.001 649.980-seq 02 0.300.001 649.980-seq 03 600.001 949.980-seq 04 900.001 1.249.980-seq 05 1.500.001 1.549.980-seq 06 1.500.001 1.849.980-seq 07 1.800.001 2.749.980-seq 08 2.100.001 2.449.980-seq 09 2.400.001 2.749.980-seq 10 2.700.001 3.049.980-seq 11 3.000.001 3.749.980-seq 12 3.300.001 3.049.980-seq 13 3.600.001 3.349.980-seq 12 3.300.001 3.649.980-seq 13 3.600.001 3.673.778 <223>-coriginal length of seq 2: 3.673778 <223>-split as follows.-seq 14 0.000.001 TO 0.349.980-seq 15 0.300.001 1.249.980-seq 16 600.001 149.980-seq 17 900.001 1.249.980-seq 18 1.200.001 1.549.980-seq 21 2.100.001 2.449.980-seq 23 2.700.001 2.449.980-seq 20 1.800.001 2.749.980-seq 21 2.100.001 2.449.980-seq 22 2.400.001 3.349.980-seq 23 2.700.001 3.449.980-seq 24 3.000.001 3.349.980-seq 25 3.300.001 3.673.778
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                                            CAAATACACAAACAACGATTATACTAAACCCAACCTAAATTTAATAATTCCGAAACAAAA
                                                                  ctaaaaccaggacacagtatactccgataccaacacaggttatcattactattacaa 1916
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AX344554.1 GI:18492440
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                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                       /note="chemically treated genomic DNA (Homo sapiens)-Original length of seq 1: 3.673778 <223>-split as follows.-seq 01 0.000.001 TO 0.39.990-seq 02 0.300.001 649.980-seq 03 00.001 949.980-seq 04 900.001 1.500.001 1.249.980-seq 06 1.500.001 1.549.980-seq 06 1.500.001 1.849.980-seq 07 1.800.001 2.749.980-seq 08 2.100.001 2.449.980-seq 07 1.800.001 2.749.980-seq 10 2.700.001 3.049.980-seq 11 3.000.001 3.749.980-seq 12 3.300.001 3.649.980-seq 31 3.000.001 3.349.980-seq 12 3.300.001 3.649.980-seq 13 3.600.001 3.673.778 <223>-original length of seq 2: 3.673778 <223>-original length 0.000.001 TO 0.349.980-seq 15 0.300.001 649.980-seq 16 600.001 949.980-seq 17 900.001 1.249.980-seq 18 1.200.001 1.549.980-seq 21 2.100.001 1.849.980-seq 22 1.800.001 2.149.980-seq 21 2.100.001 2.449.980-seq 22 2.400.001 2.149.980-seq 21 2.100.001 2.149.980-seq 23 2.700.001 3.649.980-seq 23 3.000.001 3.649.980-seq 23 3.000.001 3.649.980-seq 23 3.000.001 3.649.980-seq 25 3.300.001 3.649.980-seq 26 3.600.001 3.649.980-seq 26 3.600.001
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1 (bases 1 to 1090)

Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Parfan, D., Frise, E., George, R., Conzalez, M., Guarin, H., Li, P., Liao, G., Miranda, A., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., V., Clewis, S.E., Rubin, G.M. and Celniker, S.
                                                                                                                                                                         fruit fly.
                                                                                                                                                                                                                    Drosophila melanogaster LD17744 full length cDNA. AY069454
                                                                                                                                                      Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schlegel,R., Deeds,J., Berger,A. and Zhao,X. Genes, compositions, kits, and methods for identification
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     Direct Submission
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/db_xref="taxon:9606"
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AX188346.1
                          Sequence 4041 from Patent W00142467 AX188346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Berkeley, CA 94720, US
Sequence submitted by:
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/product="LL17744p"
/protein_10="AAL38599.1"
/db_xref="GI:17862244"
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/strain="y; on bw sp"
/db_xref="taxon:7227"
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/hdb_xref="FLYBASE:FBgn0039725"
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Best Local Similarity 75.2%;
Matches 79; Conservative
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                                                                                                                                                                                                                                                                           Query Match 3.0%;
Best Local Similarity 50.2%;
                                                                                                                                                                                                                                                            Matches 157;
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                                                                                   1952 cagatttatatacttaatcgagctggacttaattagctcttagtataccaattattagtg 2011
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                   2012 ccaccatttgtgtcgctcatacacatttatttctttattttccctaattcattagactctc 2071
                                                                                                                                                     735
                                                                                                                              199
                                                                259 AAAACAAATTAAAACCCCCAACCGCACACCTACTTCCTAAATTCGCTATAATACCTAAAAC
                                                                                                                                                                                             ATTACTGACTTCCTTGAGTAGTTTTATCTGAAATCAATTAAAAGTGTATTTGTTACTT 794
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 1298)

Schlegel,R., Deeds,J., Berger,A. and Zhao,X.

Genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of cervical cancer
Patent: WO 0142467-A 4041 14-UUN-2001;

Millennium Predictive Medicine, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Olek, A., Piepenbrock, C. and Berlin, K. Diagnosis of diseases associated with the immune Patent: WO 0200928-A 96 03-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        artificial sequence.

1 (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synthetic construct synthetic construct
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/db_xref="taxon:9606"
a 201 c 373 g 21
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1, .1298
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/db_xref="taxon:35630"
/note="chemically treated genomic DNA (Homo sapiens)"
/note="chemically treated genomic DNA (Homo sapiens)"
/note="chemically treated genomic DNA (Homo sapiens)"
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pred. No. 0.00017;
0; Mismatches 156;
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Pred. No. 0.00015;
0; Mismatches 26;
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WO0200928.
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- Qy 2132 aaaaaaaaaaaaa 2144
- Db 79 AATAAAAAACAAA 67

Search completed: July 25, 2002, 09:08:40 Job time: 11330 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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    (tgsped_patents_NA:)
1: /cgn2_6/ptodata/2
2: /cgn2_6/ptodata/2
3: /cgn2_6/ptodata/2
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Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-150-741-1
US-09-150-741-1
US-09-150-741-8
US-08-722-126A-4
US-07-945-288-9
US-08-461-809-9
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US-08-461-441-9
PCT-US93-08518-9
US-09-247-370-8
US-09-247-3730-5
US-09-247-3738-33
US-09-247-373B-33
US-09-247-373B-33
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US-08-175-928-34
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S196333-3
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US-08-460-040-1
S196333-3
US-08-48-930-13
US-08-48-930-13
US-08-48-930-13
US-08-48-930-13
US-08-3349-1
US-08-330-903A-B
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5686.010 Million cell updates/sec
                         Sequence 4, Apr-
Sequence 1, Appli
Sequence 1, Appli
Patent No. 5196333
Sequence 52, Appl
Sequence 13, Appl
Conuence 26, Appl
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ALIGNMENTS		4 US-09-262-	2 US-08-582-298-		2 US-08-668-	1 US-08-131-365в-	1212 4 US-09-222-851-18	2 US-09-092	ω	2280 3 US-08-813-150-1 Sequence	٢		4 US-08-123-934A-5	4 US-09-	2409 4 US-09-
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEPAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                        Query Match 2.8%;
Best Local Similarity 70.8%;
Matches 80; Conservative
                                                                                                                                                                                   LENGTH: 8920 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Stewart, Thomas S
APPLICANT: Flores, Maria V
APPLICANT: O'Sullivan, William J
TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
TITLE OF INVENTION: phosphate synthetase II
NUMBER OF CECURACE. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
2030 atacacatttatttcttattttccctaattcattcattagactctcatattcttaaaaagaata 2089
                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: Mitchard, Leonard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1100 No CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29.009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/446,855A FILING DATE: 06-Jul-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
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                                                             Score 60.2; DB 2;
Pred. No. 9.6e-06;
0; Mismatches 33;
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                                                                                                        Length 8920;
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; ORGANISM: Plasmodium falciparum
US-09-150-741-1
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SEQ ID NO 1
LENGTH: 8920
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                                                                                                                                                                                                                                                                                                                                                                          Patent No. 6034227
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 80;
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Best Local Similarity
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TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate
Patent No. 6183996
TITLE OF INVENTION: Synthetase II
                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: 08/446,855
EARLIER FILING DATE: 1995-07-06
NUMBER OF SEQ ID NOS: 15
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EARLIER FILING DATE: 1992-12-16
EARLIER APPLICATION NUMBER: A093/00617
EARLIER FILING DATE: 1993-12-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/150,741 CURRENT FILING DATE: 1998-09-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE:
            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA RELEASE #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/722,126A
                                                                                                                                                                                                               NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C
                                                                                                                                                                                                                                                                APPLICANT: GUTHMANN, MARCELO D.

APPLICANT: TAL, MICHAEL

TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL

TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2030 atacacatttatttcttattttccctaattcattagactctcatattcttaaaaagaata 2089
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                                                                                                                                                     COUNTRY:
                                                                                                                                                                                   CITY: Washington
                                                                                                                                                                                                     STREET:
                                                                                                                                        ZIP:
                                                                                                                                      20004
                                                                                                                                                                                                                                                                                                                                                                                            Application US/08722126A
                                                                                                                                                                    D.C.
                                                                                                                                                                                                   419 Seventh Street N.W.,
                                                                                                                                                     UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                          PECHT, Israel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
UMBER: US/08/722,126A
08-OCT-1996
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US-08-722-126A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                           APPLIANCE DATE: 06-AFR 1...
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109
APPLICATION ON-APR-1994
TOTAL DATE: 08-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
        FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,
                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2013 caccatttgtgtcgctcatacacatttatttcttattttccctaattcattagactctca 2072
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FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA FEATURE:
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                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                             CITY: Washington
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54..617
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                                                                       IL 109257
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Pred. No. 4.8e-06;
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REFERENCE/DOCKET NUMBER: PECHT-1 PCT

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CT-US95-04258-4
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             APPLICATION NUMBER: 580,655
FILING DATE: 11 SEPTEMBER 1990
APPLICATION NUMBER: 458,642
FILING DATE: 13 FEBRUARY 1990
ATTORNEY/AGENT INFORMATION:
NAME: MANDRAGOURAS, AMY E.
REGISTRATION NUMBER: F86,207
REFERENCE/DOCKET NUMBER: IFC-010CC (IMI-024)
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELEFAX: 202-737-3528
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LENGTH: 1461 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                              FILING DATE: 1992091
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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ADDRESSEE: LAHIVE & COCKFIELD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: CLONING AND SEQUENCING OF ALLERGENS FROM TITLE OF INVENTION: DERMATOPHAGOIDES (HOUSE DUST MITES)
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Local Similarity 65.9%;
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC
SOFTWARE: ASCII TEXT
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TELEFAX: (617) 227-5941
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Pred. No. 4.8e-06;
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; Patent No. 5552142
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Best Local Similarity 68.7%;
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                                                                                                        INFORMATION FOR SEQ 1D NO: 9
INFORMATION FOR SEQ 1D NO: 9
SEQUENCE CHARACTERISTICS:
SEQUENCE 1172 base pairs
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                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: IPOTELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 580,655
FILING DATE: 11 SEPTEMBER 1990
APPLICATION NUMBER: US 458,642
FILING DATE: 13 FEBRUARY 1990
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
FILING DATE: 10 SEPT
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MOLECULE TYPE:
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OPERATING SYSTEM:
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LOCATION: 1..738
                                                                                                                                                                                                                                                                                                                                                                                                              NAME: MANDRAGOURAS, AMY E. REGISTRATION NUMBER: 36,20
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                                                                                                    TYPE: nucleic acid
                                        TOPOLOGY:
                                                                    STRANDEDNESS:
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SYSTEM: PC-DOS/MS-DOS
                                        linear
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Pred. No. 2e-05;
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US-08-461-809-9
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; LOCATION:
US-08-462-831-9
                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 07/945,288
APPLICATION NUMBER: US 07/945,288
FILING DATE: 10 SEPTEMBER 1992
APPLICATION NUMBER: US 580,655
FILING DATE: 11 SEPTEMBER 1990
APPLICATION NUMBER: US 458,642
FILING DATE: 13 FEBRUARY 1990
ATTORNEY/AGENT INFORMATION:
NAME: MANDRAGOURAS, AMY E.
REGISTRATION NUMBER: 19C-010CC (IMI-024)
TELECOMMUNICATION INFORMATION:
  Matches
                 Best
                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application Patent No. 5770202
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                                                                                                                                                                                                           TELEFAX: (617) 227-59
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2030 atacacatttatttcttattttccctaattcattagactctcatattcttaaaaagaata 2089
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                  NAME/KEY:
LOCATION:
              Local
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                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                           TOPOLOGY:
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              Similarity
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  Conservative
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68.7%;
             2.7%;
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             Score 57.4;
Pred. No. 2e
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  Mismatches
             2e-05;
                         DB 1;
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                          Length 1172;
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Gaps
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                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/945,28
FILING DATE: 10 SEPTEMBER 1992
APPLICATION NUMBER: US 580,655
FILING DATE: 11 SEPTEMBER 1990
APPLICATION NUMBER: US 458,642
ETLING DATE: 13 FEBRUARY 1990
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                             2030 atacacatttatttcttattttccctaattcattagactctcatattcttaaaaagaata 2089
1019 AGACAATTTCTTATATGATTGTCACTAATTTATTTAAAAATCAAAATTTTTAGAAAATGAA 1078
                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1172 base pairs
                                                                                                                                                                                                                                                               FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
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LOCATION:
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CITY: E
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                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: MANDRAGOURAS, AMY E. REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
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                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                           nucleic acid
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60 STATE STREET, SUITE 510
                                                                                                                                                                                                                                                                                                                                                                                          5: (617) 227-7400
(617) 227-5941
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                                                                                                                              Conservative
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                              2.7%;
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                                                                                                                                            Score 57.4; DB 1; Length 1172; Pred. No. 2e-05;
                                                                                                                            0; Mismatches
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                                                                                                                            36;
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             Sequence 8, Application US/09092770
Patent No. 5973119
GENERAL INFORMATION:
APPLICANT: Coats, Steven R.
APPLICANT: Bass, Michael B.
APPLICANT: ROBINSON, Murray O.
TITLE OF INVENTION: No. 5973119el Cyclin E Genes and Proteins
FILE REFERENCE: A-524
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application PC/TUS9308518 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       Matches
CURRENT APPLICATION NUMBER: US/09/092,770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IPC-010CC (IMI-024)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                    1019 AGACAATTTCTTATATGATTGTCACTAATTTATTTAAAAATCAAAATTTTTAGAAAATGAA 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/945,288
FILING DATE: 10 SEPTEMBER 1992
ATTORNEY/AGENT INFORMATION:
NAME: MANDRAGOURAS, AMY E.
                                                                                                                                                                                                                                                                                                                                2030 atacacatttatttcttattttccctaattcattcattagactctcatattcttaaaaagaata 2089
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: cDNA
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02109
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                                                                                                                                                                                                                                                                                                                                                                                  Score 57.4; DB 5; Length 1172; Pred. No. 2e-05; 0; Mismatches 36; Indels 0
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US-09-222-851-8
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; ORGANISM: Human
US-09-092-770-8
                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 1215
TYPE: DNA
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NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 1215
                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09222851 Patent No. 6165753
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Best Local Similarity 30.6%; Pred. No. 2e-05;
Matches 112; Conservative 68; Mismatches 180;
                                                                                     Matches 112;
                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/222,851
CURRENT FILING DATE: 1998-12-30
EARLIER APPLICATION NUMBER: 09/092,770
EARLIER FILING DATE: 1998-06-05
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Coats, Steven R.
APPLICANT: Hass, Michael B.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: No. 6165753el Cyclin E Genes and Proteins
FILE REFERENCE: A-524
1593 aagctg 1598
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                                                                                   Conservative 68;
                                                                                                    2.7%;
                                                                                Score 57.4; DB 4;
Pred. No. 2e-05;
8; Mismatches 180;
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US-09-342-681C-12

; Sequence 12, Application US/09342681C

; Patent No. 6355782
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            US-09-111-730-5

; Sequence 5, Application US/09111730

; Patent No. 6274359
                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (260)..(1606)
; NAME/KEY: misc_feature
; LOCATION: (2961)..(3673)
; OTHER INFORMATION: n represents a, c,
US-09-342-681C-12
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                                                                             RESULT 13
GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/112,366 PRIOR FILING DATE: 1998-12-15 NUMBER OF SEQ ID NOS: 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Zonana et al.
TITLE OF INVENTION. Hypohydrotic ectodermal dysplasia genes and FILE REFERENCE: 52978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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Pred. No. 4.3e-05;
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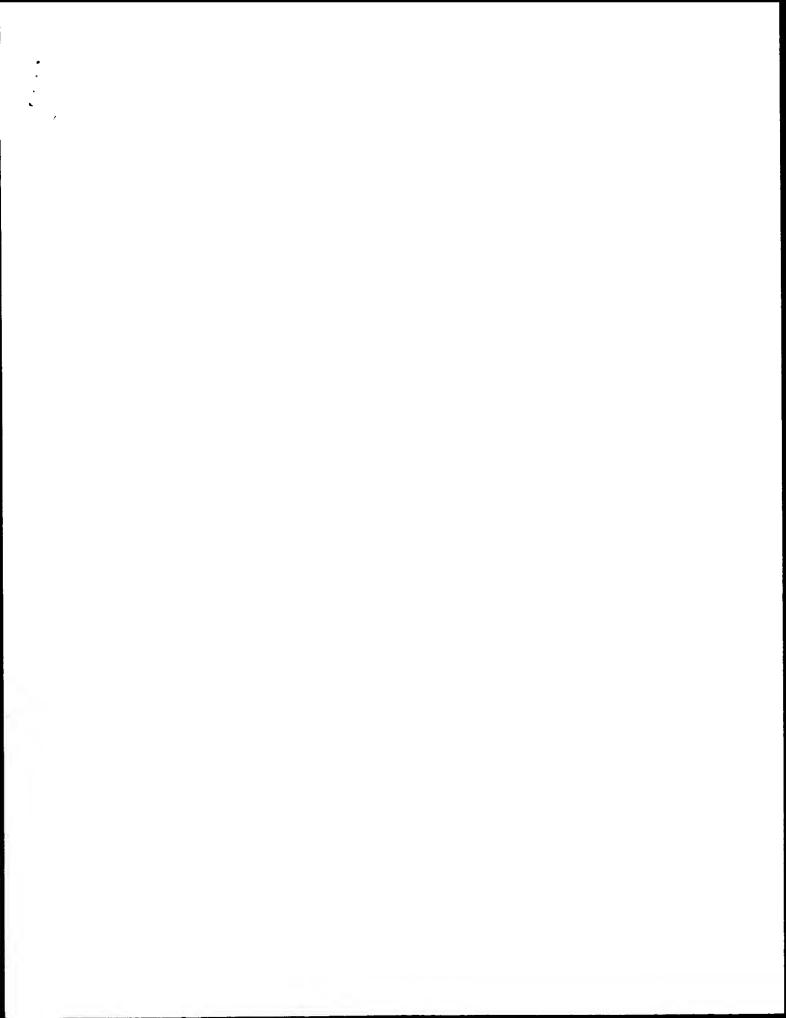
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; LOCATION: (24)..(1526)
US-09-111-730-5
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EARLIER FILING DATE: 1997-September-05
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Microsoft Word Version 7.0A
SEQ ID NO 51
LENGTH: 967
TYPE: DNA
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                                                               Query Match
Best Local Similarity
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APPLICANT: O'KEEF, DANIEL
TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1128-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Takao Saruta
APPLICANT: Hiromichi Suzuki
APPLICANT: Hiromichi Suzuki
TITLE OFI INZENTION: 25-HYDROXYVITAMIN D3-1a-HYDROXYLASE AND DNA ENCODING THE HYDRO
FILE REFERENCE: 1074
CURRENT APPLICATION NUMBER: US/09/111,730
CURRENT FILLING DATE: 1998-07-08
RUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/248,335
CURRENT FILING DATE: 1999-02-10
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APPLICANT:
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TYPE: DNA
                                                                                                                                                    ORGANISM: maize
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Conservative
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                                                               2.6%;
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                                                  Score 56.4; DB 3;
Pred. No. 3.3e-05;
0; Mismatches 36;
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Pred. No. 4.5e-05;
                                                Mismatches
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SOFTWARE: Microsoft Office 97

SEQ ID NO 33

LENGTH: 1117

TYPE: DNA
ORANISM: SOYBEAN
FEATURE:
NAME/KEY: unsure
LOCATION: (1101)
OTHER INFORMATION: M-A OR C
NAME/KEY: unsure
LOCATION: (1104)
OTHER INFORMATION: M-A OR C
NAME/KEY: unsure
LOCATION: (1116)
OTHER INFORMATION: M-A OR C
NAME/KEY: unsure
LOCATION: (1116)
OTHER INFORMATION: N-G OF A OF T OF C
US-09-247-373B-33
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US-09-247-373B-33
; Sequence 33, Application US/09247373B
; Patent No. 6168954
; GENERAL INFORMATION:
Search completed: July 25, Job time: 11390 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEFE, DANIEL
TITLE OF INVENTION: SOVEBAN GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1108-A
CURRENT APPLICATION NUMBER: US/09/247,373B
CURRENT FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 08/924,747
PRIOR APPLICATION NUMBER: 08/924,747
PRIOR TILING DATE: 1997-09-05
NUMBER OF SEQ ID NOS: 56
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Result
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Maximum Match 1008
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                           Score
 78.4
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Human immune syste		24	6535	2.9	61.2	σ
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Human colorectal c		22	216	2.9	62	w
digestive		22	216	2.9	62	່ວ
cervical		22	268	2.9	62.8	-
Human PRO4063 (UNQ	AAF44128	22	1701	2.9	63.2	0

ALIGNMENTS

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Meiotic prophase I; chromosome 1; male sterile SDS mutant; apomixis; plant breeding; seed production; SDS protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana SDS cDNA
                                                      31-MAR-2000; 2000US-193523P
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Sequence pathway. The SDS protein.

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The patent discloses novel plant gene from Arabidopsis thaliana, designated SDS, which is associated with a failure to maintain homologue attachment during meiotic prophase I. The SDS gene is located on chromosome I and is useful in plant breeding to produce male sterile SDS mutants and cloned progeny by apomixis where meiosis is bypassed in seed production. The gene may also be used as a probe to identify related genes in other plant species, and to identify and isolate other genes of the meiosis regulatory pathway. The present sequence is a CDNA encoding Arabidopsis thalians.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A new plant gene from Arabidopsis, are associated with inability to production of male sterile plants
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                       The patent discloses novel plant gene from Arabidopsis thaliana, designated SDS, which is associated with a failure to maintain homologue attachment during meiotic prophase I. The SDS gene is located on chromosome I and is useful in plant breeding to produce male sterile SDS mutants and cloned progeny by apomixis where meiosis is bypassed in seed production. The gene may also be used as a probe to identify related genes in other plant species, and to identify and isolate other genes of the meiosis regulatory pathway. The present sequence is SDS gene from Arabidopsis thaliana
                                                                                                                                                                                                             A new plant gene from Arabidopsis, designated SDS, mutations in are associated with inability to produce pollen, is useful for production of male sterile plants for plant breeding .
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                                                                                                 actgcatcagcccactctctagtctctgactaacgaacttccattttcaaaattcgaatt 2955
                                                            tctaatttctagtttcaagctttcgtacggagaaaaatgaaggagatcgcgatgaggaa 120
                                               tctaatttctagtttcaagctttcgtacggagaaaaaatgaaggagatcgcgatgaggaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ttttggatcttcttgcgaggaagaaattcactctgaatt 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ttttggatcttcttgcgaggaagaaattcactctgaagt 1628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UNIV PENNSYLVANIA STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prophase I;
3018
                                                                                                                                                                                                                  3018 BP; 996 A; 529 C; 476 G;
                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001WO-US09875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome 1; male sterile SDS mutant; apomixis;
                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     production; SDS protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDS promoter
                                                                                                                                                                                                                                                                                                                                                                                      47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3018
                                                                                                                                                     0;
                                                                                                                                                                           Score 123;
                                                                                                                                                                 Pred. No.
                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA
                                                                                                                                                                                                                                                       promoter DNA from
                                                                                                                                                    . 9.1e-16; ches 0;
                                                                                                                                                                                                                  1017 T; 0 other;
                                                                                                                                                                             В
                                                                                                                                                                             22;
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                                                                                                                                                                          Length 3018;
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                                                                                                                                                  Gaps
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Best Local
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                            2387
                                                     1953
                                                                                                         1893
  2013
                                                                                2447
                                                                                                                                                             1833
                                                                                                                                                                                                                                                                            including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myelo leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                     Sequence 5204 BP; 1463 A; 72 C;
                                                                                                                                                                                                                                                                                                                                          can be used in the diagnosis and treatment of immune system disorders,
                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 874; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosts; anaemia; acute myeloid leukaemia; Alpheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease
                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL32901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABL32901 standard; DNA; 5204
caccatttgtgtcgctcatacacatttatttcttattttccctaattcattagactctca
                                                                                             2002-130909/17.
                          agatttatatacttaatcgagctggacttaattagctcttagtataccaattattagtgc
                                                                            166;
                                                                                                                                                                                                                                                                                                                                                            which are modified by the methylation of cytosines.
                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Piepenbrock C,
                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000DE-1032529
2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                 3.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 associated
                                                                                                                                                                                                                                                                                                                                                          provides a number of human immune system associated ied by the methylation of cytosines. The sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berlin
                                                                                                                                                                                      0;
                                                                                                                                                                                                 Score 78.4;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВP
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                                                                                                                                                                                                                                                     1014 G;
                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>~</u>
                                                                                                                                                                                                                                                    2655 T; 0 other;
                                                                                                                                                                                                DB 24;
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                                                                                                                                                                                                             Length 5204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    epilepsy;
bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                           abnormal
                                                                                                                                                                                                                                                                                                                      acute myeloid
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AAH70126/c
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Best Local S
Matches 91
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09-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cervical cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH70126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2207
                                                                                                                                                                                                                                                                                    Claim 1; Page 319-320;
                                                                                                                                                                                                                                                                                                                                                                      Schlegel
                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cervical cancer marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-SEP-2001
                       2038
                                                                                                                                                                                      cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be
                                                                                                                                                                                                                                    cervical cancer with cytostatic activity. The nucleic acids and en polypeptides are useful: to assess if a patient is afflicted with
                                                                                                                                                                                                                                                             The invention relates to novel genes (AAH68727-AAH73383) associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-DEC-1999;
                                                                                                                                                    Sequence 545 BP; 200 A; 40 C; 23 G;
                                                                                                                                                                                                                                                                                                                                                                                            (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                             userur for gene therapy.
 220
                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                       isolated nucleic acid for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ttatttcttattttccctaattcattagactctcatattcttaaaaagaatatttccttg
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                                                                                                                                                                                                                                                                                                           assessing and
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                                                                                            Conservative
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2000US-0203791.
2000US-0210600.
2000US-0220114.
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                                                                                                                                                                                                                                                                                                                                                                      Deeds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0169681
99US-0171350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic; pre-malignant condition; gene therapy; ss
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                                                                                                       3.0%;
54.5%;
                                                                                                                                                                                                                                                                                                           detecting compounds for treating the
                                                                                                                                                                                                                                                                                   1051pp;
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                                                                                           0;
                                                                                                       Score 63.4; DB 2
Pred. No. 0.00092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid 1400
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                                                                                                                                                                                                                                                                                    English.
                                                                                            Mismatches
                                                                                                                                                     209 T;
                                                                                                                                                                                                                                                                                                                       and treating cervical cancer
                                                                                                                  DB 22;
                                                                                                                                                     73 other;
                                                                                            76;
                                                                                                                 Length 545;
                                                                                            Indels
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12-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                        The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for this time are cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-DEC-1999;
21-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH72764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH72764 standard; cDNA; 1298
                       2040 atttcttattttccctaattcattagactctcatattcttaaaaagaatatttccttgtt 2099
                                                                                                                                                              Sequence 1298 BP;
                                                                                                                                                                                                                                                                                                    Claim 1; Page 838-839; 1051pp; English.
                                                                                                                                                                                                                                                                                                                                                                                          Schlegel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200142467-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cervical cancer marker nucleic acid 4038.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160
                                                                                                                                                                                                  inhibiting cervical cancer in a patient. The nucleic acids may also
 735 attactgactttccttgagtagtttttatctgaaatcaattaaaagtgtatttgttactt 794
                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               σ
                                                                                                                                                                                                                                                                                                                                          isolated nucleic acid for diagnosing and treating cervical cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                             assessing and detecting compounds for treating the cancer
                                                                                                                                                                                       gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0189315.
2000US-0203791.
2000US-0210600.
2000US-0220114.
                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                          Deeds J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000WO-US33312
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99US-0171350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic;
                                                                                                                                                              507 A; 201 C;
                                                                                                           3.0%;
                                                                                                                                                                                                                                                                                                                                                                                          Berger
                                                                                                  0,
                                                                                              Score 63.4; DB zz;
Pred. No. 0.0011;
"""matches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pre-malignant condition;
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                                                                                                                                                              373 G; 215 T;
                                                                                                                                                               2 other;
                                                                                                                        Length 1298;
839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene therapy;
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ABL32123/c ID ABL321 XX

ABL32123 standard; DNA;

6564 BP

RESULT

ABL32123;

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Best Local :
                                                                                                                                                                                                                                                                                              Best Local Similarity Matches 157; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, NIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                             1832 taagcaatcaaaaagaacaaaaaccctaaaaccaggacacagtatactccgataccaaca 1891
                          1892 cacaggitatcattactatttacaaaaacaaacacaaggiaagtaataagaactcctcta 1951
                                                                                                                                                                                                                                                                                                                                                                     Sequence 6564 BP; 1603 A; 97 C; 1773 G; 3091 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antitheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUN-2000;
01-SEP-2000;
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   139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid comprising fractor diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acute myeloid leukaemia; Alzheimer's disease; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
                                                            199
                                                                                                                                                                               319
cagatttatatacttaatcgagctggacttaattagctcttagtataccaattattagtg
                                                                                     ccaccatttgtgtcgctcatacacatttatttcttattttccctaattcattagactctc
                                                                                                                                                                         GCCACTCTTAAAAATCTAACCTCCCTTAAAAATATATAACCTCTAATTAATTATAAAACA
                                                                                                                 AAAACAAATTAAAACCCCCAACCGCACACCTACTTCCTAAATTCGCTATAATACCTAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immune system associated gene SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Piepenbrock C,
                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000DE-1032529
2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ID NO 96; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001WO-EP07537.
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                                                                                                                                                                                                                                                                                                                                                                                                  present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                           3.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fragment of chemically modified ment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Berlin
                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                           Score 63.4; DB:
Pred. No. 0.0014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arthritis; psoriasis; bowel disease,
                                                                                                                                                                                                                                                                                              Mismatches 156;
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                                                                                                                                                                                                                                                                                                                         24;
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                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                       Length 6564;
                                                                                                                                                                                                                                                                                                                                                                     other;
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                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                            Gaps
 80
                                                        140
                                                                                     2071
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2045 ttattttccctaattcattagactctcatattctttaaaaagaatatttccttgtttgaaa 2104

Matches

Local Similarity

2.9%;

Score 63.2; DB 2 Pred. No. 0.0012;

DB 22; 23;

Length Indels

6

0;

Gaps

Conservative

0

Mismatches

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SON COCCCCCXX PART PROXX PROXX
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18-FEB-2000;

18-FEB-2000;

22-FEB-2000;

01-MAR-2000;

03-MAR-2000;

25-MAR-2000;
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15-SEP-1999;
07-DEC-1999;
09-DEC-1999;
11-JAN-2000;
                                                                                                                                                      The present sequence is the coding sequence for a human PRO polypeptide (secreted and transmembrane). The PRO protein, and PRO agonists, PRO antagonists or anti-PRO antibodies are useful for preparation of a medicament useful in the treatment of a condition which is responsive to the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO
     Sequence
                                                                                                  the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO protein may also be employed as molecular weight markers for protein electrophoresis. The PRO coding sequence has applications in molecular hallows in the protein sequence has applications.
                                                                                                                                                                                                                                                                                                                              Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                chromosome and gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                       Eighty four nucleic acids encoding F
molecular biology, including use as
                                                                           biology, including use as hybridisation probes, and in chromosome and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Grimaldi CJ,
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                                                    mapping.
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     1672 BP;
                                                                                                                                                                                                                                                                                                                            Fig 17; 278pp; English.
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J, Gurney AL,
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2000WO-US04341.
2000WO-US04342.
2000WO-US04414.
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2000US-0209832
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552 A; 281 C;
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Watanabe
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     367
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  472 T; 0 other;
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98US-008861. 98US-008863. 98US-0088876. 98US-0089105. 98US-0089105. 98US-0089114. 98US-0089512. 98US-0089532. 98US-0089533. 98US-0089539. 98US-0089599. 98US-0089599. 98US-0089599. 98US-0089600. 98US-0089601.	98US-008B029 98US-008B033 98US-008B326 98US-008B326 98US-008B217 98US-008B217 98US-008B722 98US-008B734 98US-008B734 98US-008B741 98US-008B741 98US-008B741 98US-008B741 98US-008B741 98US-008B741 98US-008B741 98US-008B741 98US-008B741 98US-008B741 98US-008B741 98US-008B741 98US-008B741 98US-008B741 98US-008B741 98US-008B741 98US-008B741 98US-008B741	99WO-US12252. 98US-0087607. 98US-0087759. 98US-0087827. 98US-0087827. 98US-0088025.	standard; cDNA; 1701 BP. 100 (first entry) bound protein PRO1063 encoding cDNA. bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand; Itical; receptor immunoadhesin; gene mapping; ss.	ttttctttgctaatttggaagattaactcattttaataaaattatgtctaagattaaaa 1602 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa
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26-AUG-1998;
26-AUG-1998;
26-AUG-1998;
26-AUG-1998;
26-AUG-1998;
26-AUG-1998;
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18-AUG-1998;
19-AUG-1998;
Human; secreted and transmembrane protein; PRO; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     sequences have homology with proteins including LDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceuctical and diagnostic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIE
                             Human PRO4063
                                                         02-APR-2001
                                                                                                             AAF44128 standard; cDNA; 1701 BP
                                                                                                                                                                              1632 гасадавававававававававававававававава 1671
                                                                                                                                                                                                                                                                                                                                                                                             are useful as hybridization probes, in chromosome and gene mapping and the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially
                                                                                                                                                                                                                                                                                                                                                           Sequence 1701 BP;
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24-AUG-1998;
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es 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                    recombinant techniques.
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Yuan J;
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                                                      (first entry)
                          (UNQ128) nucleotide sequence SEQ ID NO:114.
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98US-0100634.
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98US-0097978.
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98US-0097986.
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9086
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s-0097971.
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Pred. No. 0.0012;
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The present invention describes human secreted and transmembrane PRO
C proteins. The PRO proteins have cytostatic activity. The PRO proteins
C can be used for targeted delivery of bloactive molecules, such as
C toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
C toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
C sequences, and their fragments, can be used as hybridisation probes, in
C chromosomal and gene mapping, and in the generation of anti-sense RNA
C and DNA. They may also be used to produce transgenic animals which are
C used to develop and screen therapeutically useful reagents. The PRO
C nucleotide and protein sequence can be used for tissue typing and in
C treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
C AAP44270 to AAF44470 represent PCR primers and hybridisation probes used
C h the isolation of human PRO sequences. AAP44087 to AAF44269 and
C AAB65154 to AAB65300 represent human PRO polynucleotide and protein
C sequences given in the exemplification of the present invention.
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22-FEB-2000;
24-FEB-2000;
24-FEB-2000;
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26-JUL-1999;
28-JUL-1999;
17-AUG-1999;
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Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams
                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                PRO polynucleotides used bioactive molecules such
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diagnostic assay; ss.
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L-DEC-1999;
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DB; AAB65177.
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2000WO-US00376
2000WO-US03565
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2000WO-US04914
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2000WO-US06884.
2000WO-US07377.
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99WO-US28301
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99WO-US21547
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99US-0149396
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                                                                                                                                                                                                                                                               s used to produce polypeptides used to target
s such as toxins, radiolabels or antibodies,
cause targeted cell death -
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Gerber H, Gerri
                                                                                                                                                                                                                                      English.
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lliams PM,
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Godowski PJ;
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Query Match Best Local Similarity

2.9%;

Score Pred.

63.2; DB 22; No. 0.0012;

Length 1701;

Sequence 1701 BP; 557

A; 288

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381 G; 475 T; 0 other;

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RESULT 11
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                                                                                                                                          cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be useful for each therapy.
                                                                                                                                                                                                                Claim 1; Page 313; 1051pp; English.
                                                                                                                                                                                                                                                                                                                                                                          08-DEC-2000; 2000WO-US33312
                                                                                                                                                                                                                                                                                                                                                                                                            WO200142467-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                             Cervical cancer; cytostatic;
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                                                                                                                                                                                                                                                                             Schlegel R,
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14-MAR-2000;
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                                                                                                                    Sequence 268
                                                                                                                                                                                               The invention relates to novel genes (AAH68727-AAH73383) associated with
                                                                                                                                                                                                                                                                                            (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                           14-JUN-2001
                       useful for
                                                                                                                                                                                                                                                                                                                                12-MAY-2000;
                                         267
                                                                                                                                                                                                                                 isolated nucleic acid for diagnosing and treating cervical car
for assessing and detecting compounds for treating the cancer
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                                         AAAAANTTTTTTTNNANNTTTTTTTTTTTTCCCCCCTTTNNTAAAGAATTTTTTTNNAAA
                                                                           103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77;
                                                                                    Similarity
                                                                                                                                    gene therapy.
                                                                                                                                                                                                                                                                                                             99US-0171350.
2000US-0189315.
2000US-0203791.
2000US-0210600.
2000US-0220114.
                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                    BP; 62
                                                                                                                                                                                                                                                                                                                                                          99US-0169681
                                                                                                                    A; 10 C;
                                                                                  2.9%;
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                                                                          0
                                                                                  Score 62.8; DB Pred. No. 0.0011
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                                                                                                                                                                                                                                                                                                                                                                                                                                             pre-malignant condition; gene therapy;
                                                                           Mismatches
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                                                                                                                     142 T;
                                                                                          DB 22;
                                                                                                                     37 other;
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                                                                                           Length
                                                                                             268;
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18-APR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
                                                        14 - AUG - 2000

17 - AUG - 2000

18 - AUG - 2000

22 - AUG - 2000

22 - AUG - 2000

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01 - SEP - 2000
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14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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26-JUL-2000;
26-JUL-2000;
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24-FEB-2000;
02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; digestive system antigen; gene therapy; cancer; ulcerative colitis; infection; Hirschsprung's disease; digestive system disorder; Meckel's diverticulum; ss.
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11-JUL-2000;
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2000US-02117496.
2000US-022963
2000US-0229513
2000US-0224518
2000US-0225214
2000US-0225214
2000US-0225214
2000US-0225266
2000US-0225277
2000US-0225477
2000US-0225477
2000US-0225487
2000US-02257757
2000US-0225759
2000US-0225759
2000US-0227758
2000US-0225759
2000US-0227798
2000US-0227798
2000US-0227799
2000US-0227799
2000US-0226681
2000US-0227799
2000US-0226681
2000US-02279934
2000US-0229343
2000US-0229344
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2000US-0205515.
2000US-0209467.
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2000US-0186350.
2000US-0189874.
2000US-0190076.
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2000US-0216880.
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2000US-0215135.
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chronic colit
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PR 06-SEP-2000 2000US-0231443
PR 09-SEP-2000 2000US-0231444
PR 09-SEP-2000 2000US-0231444
PR 09-SEP-2000 2000US-0231441
PR 09-SEP-2000 2000US-0231460
PR 114-SEP-2000 2000US-0231460
PR 21-SEP-2000 2000US-02314
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RESULT 1
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Best Local Similarity bz...
">+ches 95; Conservative
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17-NOV-2000
17-NOV-2000
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05-DEC-2000
05-DEC-2000
05-DEC-2000
06-DEC-2000
08-DEC-2000
                                                                                                                                                                                                                                               1993
                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a cDNA encoding a digestive
       Human colorectal cancer antigen cDNA SEQ ID NO:
                               19-OCT-2001
                                                                                                                                2053
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders o digestive system, particularly cancer and cancer metastases -
                                                     AAI57565;
                                                                          AAI57565 standard; cDNA;
                                                                                                                                                                                                                                                                                                                        Sequence 216 BP; 103 A; 24 C; 26 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
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DB; AAM92541.
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                                                                                                                                                                                                                                                                                                                                               antigen of the invention.
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2000US-0249244
2000US-0249264
2000US-0249264
2000US-0249296
2000US-0249299
2000US-0249299
2000US-0250160
2000US-0250160
2000US-0251983
2000US-0251986
2000US-0251868
2000US-0251868
2000US-0251869
2000US-0251869
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2000US-0251869
2000US-0251869
                             (first entry)
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                                                                                                                                                                                                                                                                             2.9%;
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                                                                                                                                                                                                                                                                  ; Score 62; DB
; Pred. No. 0.00
1; Mismatches
                                                                          ВР
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                                                                                                                                                                                                                                                                                                                         60 T; 3 other;
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	21-SEP-2000;	SEP-2000;	SEP-2000;	SEP-2000;	SEP-2000;	SEP-2000:	SEP-2000	SEP-2000,	2000	SEP-2000;	SET - 2000;	SEP-2000;	SEP-2000;	SEP-2000;	SEP-2000;	AUG-2000;	-Aug-2000;	2-AUG-2000;	2-AUG-2000	2-AUG-2000	8-AUG-2000	-AUG-2000	-AUG-2000	14-AIIG-2000;	- AUG - 2000	-AUG-2000	-AUG-2000	AUG-2000	14 - AUG - 2000;	AUG-2000	14-AUG-2000;	301G-2000	26-JUL-2000;	JUL-2000	JUL - 2000	11-JUL-2000;	07-JUL-2000;	30-JUN-2000;	28-JUN-2000;	07-JUN-2000	19-MAY-2000;	17-MAR-2000;	16-MAR-2000;	02-MAR-2000	24-FEB-2000	31-JAN-2000;	001	17-JAN-2001.	02-AUG-2001	WOZOCIOSSO-	100001110	Homo sapiens	Human; colo									
	2000US-0234274.	2000US-0234223.	2000US-0233064.	2000US-0233063.	200008-0232401.	200005-0232399.	2000US-0232398.	2000US-0232397.	2000US-0231968.	2000US-0232081.	2000US-0232080.	2000US-0231414.	2000US-0231413	200005-0231244	200005-0231242.	200003-0230430.	200005-0230437.	2000US-0229513.	200008-0229509.	20000S-0229345.	200008-0229344.	20000S-0229343.	2000US-0229287.	2000US-0228924.	2000US-0227009.	2000US-0227182.	2000US-0226868	2000US-0226681	2000US-0226279	2000HS-0225759	200005-0225757	200003-0225447.	200008-0225270.	2000US-0225268.	2000US-0225267.	2000US-0225266.	2000US-0225214.	200005-0224519.	200008-0224518.	200005-0220964.	2000US-0220963.	2000US-0218290.	2000US-0217496.	200003-0216880.	2000US-0216647.	2000US-0215135.	2000US-0214886.	2000US-0209467	2000US-0198123.	2000US-0190076.	2000US-0189874.	2000US-0186350.	200005-0184664	2000US-0179065.	FOOTMO-OSOTSSO.		•	-A1.			colorectal cancer; col	
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PR	PR	PR	PR	מ ק	PR	PR	PR:	יי כי כי	בי גני	ָּבְיבָּ בּבְיבָ	27	PR	PR	PR	PR	PR	PR	PR	PR	PR	PR	PR	P	מ ק	בר ג	ָ קלא	PR	PR	PR	PR	PR	PR	PR	PR :	יי קל	בי א ל	PR	PR	PR	PR:	ת ק	, T	PR	PR	PR	בי גם	PR	PR	PR	יי א	יי גיט	PR	PR	קי גיק	PR	PR	אין אין	PR	PR	PR	PR	
2001;	-DEC-2000;	.2000;	2000;	. 2000:	2000;	2000;	-2000;	2000	2000;	2000;	NOV-2000;	-NOV-2000;	-NOV-2000;	-NOV-2000;	2000;	NOV-2000;	NOV-2000;	NOV-2000;	-NOV-2000:	-NOV-2000;	NOV-2000;	NOV-2000;	2000.	NOV-2000;	(0002-AON	NOV-2000;	NOV-2000;	2000;	2000;	2000;	2000;	-NOV-2000;	-NOV-2000;	NOV-2000;		NOV-2000;	NOV-2000;	NOV-2000;	000;	08-NOV-2000;		2000;	2000;	0-OCT-2000;	000	2000	0-OCT-2000;	000;	000		000	000	000	000	29-SEP-2000;	000	0000	000		000	2000	
25	2000US-0251990. 2000US-0254097.	25	25	2 6	25	25	25	2 7	100	24	24	24	24	24	24	24	24	22	22.	24	24	22.	2 4	2.4	224	024	024	024	024	024	024	024	22	024	2 6	024	024	024	024	024	02464/4	0244617	0241826	024	0241/0/	0241786	0241785	0241221	0240960	35	02	02	02	0 0	02	02	02	02	3 6	202	02	

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 number of colorectal cancer antigens. These are shown in AAI57547-AAI57619 and AAM38569-AAM38641. These can be used in the diagnosis, prevention and treatment of cancer of the colon and/or rectified the present sequence is a colorectal cancer antigen coding sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the colon and rectum including colorectal cancers and also for testing and detection e.g. diagnosis - \frac{1}{2}
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                                                                                                                                                       09-AUG-2001
                                                                                                                                                                                                                                                        Differential transcription; human; rat; tumour cell; cytostatic;
                                                                                                                                                                                                                                                                                  Rat differential transcription-associated cDNA SEQ ID 630
                                                                                                                                                                                                                                                                                                               21-SEP-2001
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WPI; 2001-483415/52
                                                                                               31-JAN-2000; 2000DE-1004102.
                                                                                                                           31-JAN-2001; 2001WO-EP01003
                                                                                                                                                                                  WO200157058-A2
                                                                                                                                                                                                                                          Ras modulator; Class II tumour suppressor gene; gene therapy; ss
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                                     Rosenthal A,
                                                                  (META-) METAGEN GES GENOMFORSCHUNG MBH
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                                        Hinzmann
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                          Schaefer R, Zu
Shmitz A, Sers

    Mismatches

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ers C;
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     targets for diagnosis or therapy and in screening to determine the effects of an active compound (potential pharmaccutical) on a cell line, particularly for diagnosis and treatment of tumors, especially by modulating expression of (I) (by gene therapy, antisense RNA or ribozyme methods) or by modulating the amount and/or location of (I)-encoded polypeptides (by administration of the polypeptide or its activator, antibody (optionally as a conjugate) or inhibitor). The method allows identification of many class II tumour suppressor genes (i.e. genes that are not primary targets for tumour-initiating mutations). AAH80149-AAH82376 represent the human and rat derived nucleic acid fragments described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a nucleic acid (I) with differential expression between tumour and normal cells and which has cytostatic activity. (I) work as modulators of Ras activity by inducing expression of tumour suppressor genes. (I), and polypeptides encoded by them, are useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids differentially expressed between tumor and normal cells, useful for diagnosis or therapy of tumors and for screening active
                                                                                                                                                                          29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                       03-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH33177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH33177 standard; cDNA; 705 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2041 tttcttattttccctaattcattagactctcatattcttaaaaagaatatttccttgttt 2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 255 BP; 74 A; 26 C; 43 G; 102 T; 10 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Page 532-533; 579pp; German
                                                                                                                                                                                                                                                                                        WO200122920-A2
                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                   Human colon cancer antigen encoding cDNA SEQ ID NO:233.
                                                           P-PSDB; AAG73746
                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                           05-APR-2001
                                                                                                                                                                                                                                                                                                                                                         colorectal carcinoma; ss.
                                                                                                                                                                                                                                                                                                                                                                       Human; colon cancer; colon
                                                                                                            Ruben SM,
                                                                                                                                                                                                                         28-SEP-2000; 2000WO-US26524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 TTTATTTTTTTKTTTTKGGCATTATAMCCTTTTTTTTTTTTTTTAAATTTTCCCTTTTGG 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                              2001-235357/24.
                                                                                                           Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                          99US-0163280
                                                                                                                                                                                           9908-0157137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.9%;
                                                                                                            Birse CE,
                                                                                                                                                                                                                                                                                                                                                                       cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 62;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                              Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.0016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22; Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -

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                                                                                                                                                                                                                                                                                                                                                                                     CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon CC cancer associated nucleic acid molecules (N) and proteins (P), where CC the proteins are collectively known as colon cancer antigens. The colon CC cancer antigens have cytostatic activity and can be used in gene CC therapy and vaccine production. N and P may be used in the prevention, CC diagnosis and treatment of diseases associated with inappropriate P CC expression. For example, N and P may be used to treat disorders CC associated with decreased expression by rectifying mutations or deletions in patient's genome that affect the activity of P by expressing CC inactive proteins or to supplement the patients own production of P. CC Additionally, N may be used to produce the colon cancer associated Ps. CC by inserting the nucleic acids into a host cell and culturing the cell CC to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37194 to AAH37204 cn present invention
                                                                                                                                                                                                                                                      Query Match 2.9%; Score 62; DB 22; Length 705; Best Local Similarity 62.5%; Pred. No. 0.0018; Matches 95; Conservative 1; Mismatches 56; Indels
                                                                                                                                                                                      2113 аааааааааааааааааааааааааааааааааа 2144
                                                                                           present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                        Sequence 705 BP; 258 A; 97 C; 99 G; 247 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 2371; 9803pp; English.
                                                               519 agtatagaacttataaaccaatatattgatatttttaaaaacatttttacatataagtaaa 578
                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                      Gaps
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Search completed: July 25, 2002, 09:16:35 Job time: 8225 sec

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639 aaaaaaaaaaaaaaaaaaaaaaaaaaa 670

